## LISTING OF THE CLAIMS

1. (Currently amended) A computer implemented method for predicting the structure of a membrane-bound protein having a plurality of $\alpha$ helical regions, comprising:

~~providing an amino acid sequence for the membrane-bound protein;~~

identifying a range of amino acids in [[the]] an amino acid sequence of the membrane-bound protein as transmembrane regions of the membrane-bound protein;

constructing each of two or more helices in a set of helices for the transmembrane regions;

optimizing a helix bundle configuration for the set of helices using a first molecular dynamics simulation;

after optimizing the helix bundle configuration, constructing one or more inter-helical loops to generate a full-atom model of the membrane-bound protein; and

optimizing the full-atom model using a second molecular dynamics ~~simulation; and~~ simulation, thereby providing

~~outputting~~ a predicted structure for the membrane-bound protein ~~based on the second optimization~~.

2. (Cancelled).

3. (Currently amended) The method of claim 1, ~~wherein:~~ wherein the

constructing each of two or more helices in the set of helices for the transmembrane regions ~~includes~~ includes one or more of: constructing each of two or more canonical helices corresponding to the transmembrane regions, calculating a minimum-energy configuration for each of the canonical helices, and optimizing each of the canonical helices.

4-34. (Cancelled)

35. (Currently amended) The method of claim ~~3, wherein:~~ 1, wherein the

optimizing a helix bundle configuration ~~includes~~ includes one or more of: assembling a helix bundle including each of the set of helices, and calculating a minimum-energy configuration for the helix bundle in a lipid bilayer.

36. (Previously Presented) The method of claim 1, wherein:
the membrane-bound protein is a G-protein coupled receptor.

37. (Previously presented) The method of claim 1, wherein:
identifying a range of amino acids in the amino acid sequence as transmembrane regions includes aligning the amino acid sequence with an experimental or theoretical helical template.

38. (Previously presented) The method of claim 1, wherein:
identifying a range of amino acids in the amino acid sequence as transmembrane regions includes determining the periodicity of hydrophobic residues in the amino acid sequence; and
optimizing a helix bundle configuration includes identifying a plurality of lipid-accessible residues based at least in part on the determined periodicity.

39. (Previously Presented) The method of claim 1, wherein:
constructing each of two or more helices in a set of helices for the transmembrane regions includes optimizing each of the two or more helices in the set of helices using a torsional molecular dynamics method.

40. (Previously Presented) The method of claim 39, wherein:
the torsional molecular dynamics method uses the Newton-Euler Inverse Mass Operator.

41. (Previously Presented) The method of claim 1, wherein:
constructing each of two or more helices in a set of helices for the transmembrane regions includes determining 3-D coordinates that define the structure of each helix in the set of helices.

42. (Previously Presented) The method of claim 1, wherein:

optimizing a helix bundle configuration includes determining a rotation and tilt of each helix in the set of helices.

43. (Previously Presented) The method of claim 1, wherein:

optimizing a helix bundle configuration includes orienting the helix axes according to the 7.5 Å electron density map for rhodopsin.

44. (Previously Presented) The method of claim 38, wherein:

optimizing a helix bundle configuration includes orienting the identified lipid-accessible residues to face the outside of the helix bundle.

45. (Previously Presented) The method of claim 1, wherein:

the first molecular dynamics simulation is a rigid body molecular dynamics simulation.

46. (Previously presented) The method of claim 1, wherein:

optimizing a helix bundle configuration for the set of helices includes modeling an effect of an environment of the membrane-bound protein, wherein the effect of the environment is simulated with a continuum description of a water environment and a lipid bilayer.

47. (Currently amended) The method of claim 45, wherein:

the first molecular dynamics simulation uses the DREIDING force field, charges derived from charge equilibriation to simulate lipids in ~~simulating~~ the membrane, and charges from CHARMM22 for the membrane-bound protein.

48. (Previously Presented) The method of claim 1, wherein:

the second molecular dynamics simulation is a mixed mode molecular dynamics simulation.

49. (Currently amended) The method of claim 48, wherein:

the second molecular dynamics simulation uses a torsional molecular dynamics method to model the helices and inter-helical loops and a rigid body molecular dynamics method to model [[the]] a membrane [[of]] in which the membrane-bound protein is situated.

50. (Previously Presented) The method of claim 1, wherein:

the second molecular dynamics simulation includes dynamic optimization of the structure using cell multipole methods or fast torsional dynamic methods.

51. (Previously Presented) The method of claim 1, wherein:

at least the second molecular dynamics simulation includes a solvent approximation.

52. (Previously Presented) The method of claim 51, wherein:

the solvent approximation is a continuum solvation model.

53. (Previously Presented) The method of claim 52, wherein:

the solvent approximation includes the Surface Generalized Born model or the Poisson-Boltzmann description.

54. (Previously Presented) The method of claim 53, wherein:

the solvent approximation is an empirical approximation comprising estimating solvation free energy as a function of solvent accessible protein surface area.

55. (Currently amended) The method of claim 1, wherein:

the ~~predicted structure is generated by performing the~~ second molecular dynamics simulation is performed for a time in the range from about 100 ps to about 1 ns.

56. (Previously presented) The method of claim 1, wherein:

the set of helices includes four or more membrane-spanning α-helices.

57. (Previously presented) The method of claim 1, wherein:

the set of helices includes seven membrane-spanning α-helices.

58. (Previously presented) The method of claim 1, wherein said identifying comprises identifying ranges of amino acids in the amino acid sequence as transmembrane regions of the membrane-bound protein.

59. (New) The method of claim 50, wherein:

prior to the second molecular dynamics simulation, a full atom minimization of the full-atom model with a barrel of lipid surrounding the protein is performed.

60. (New) The method of claim 1, wherein the amino acid sequence of the membrane-bound protein is obtained from GeneBank.

61. (New) The method of claim 1, wherein the predicted structure is output in protein data bank format.

62. (New) A programmable digital computer, configured to perform the method of claim 1.